



11

SEQUENCE LISTING

<110> Padigaru, Muralidhara
Gerlach, Valerie L.
Smithson, Glennnda
Stone, David
Bin-Yang, Ruey
Conley, Pamela B.
Hart, Matthew
Tomlinson, James E.
Topper, James N.
Kekuda, Ramesh
Casman, Stacie J.
MacDougall, John R.
Shlomit, Edinger R.

<120> Novel GPCR-Like Proteins and Nucleic Acids Encoding
Same

<130> 21402-224 AG

<140> 10/024444

<141> 2001-12-18

<150> 60/256635

<151> 2000-12-18

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 977

<212> DNA

<213> Human

<400> 1

```
gcaactaaaa aaacacatca tggagctccg gaactccacc ttgggaagcg gcttcattctt 60
ggtgggggatt ctgaatgaca gtgggtctcc tgaactgctc tatgctacat ttacaatcct 120
atacatgttg gcaactgacca gcaatggtct gctgctcctg gccatcacca tagaagcccg 180
gtccacatg cccatgtacc tctgcttg gacgctctct ctcattggacc tctgtttcac 240
atctgtttgtc actcccaagg ccttggcgga ctttctgcgc agagaaaaca ctatctcctt 300
tggaggctgt gcaacttcaga tgttcctggc actgacaatg ggtagcgctg aggacctcct 360
actggccttc atggcctatg acaggatatgt ggccatttgt catcctctga aatacatgac 420
cctcatgagc ccaagagtct gctggatcat ggtggccaca tcctggatcc tggcatccct 480
gattgctata ggacatacca tgtacactat gcacctccct ttctgtgtgt cctgggaaat 540
caggcatctg ctctgtgaga tcccaccctt gctgaagttg gcctgtgctg atacctccag 600
gtatgagctt ataataacg tgacaggtgt gactttcctc ttgctcccca tttctgccat 660
tgtggcctcc tacacactag tctattcac tgtgcttcgt atgccatcaa atgaggggag 720
gaagaaagcc cttgtcacct gctcttccca cctgattgtg gtcgggatgt tctatggagc 780
tgccacattc atgtatgtct tgcccagttc cttccacagc cccaaacaag acaacatcat 840
ctctgttttc tacacaattg tcaactccagc cctgaatcca ctcatctaca gcctgaggaa 900
taaggaggtc atgctgggct tgaggagggt cctgggaaaa tacatactgc tggcacattc 960
cacgctctag ggaagga                                     977
```

<210> 2

<211> 316
 <212> PRT
 <213> Human

<400> 2

```

Met Glu Leu Arg Asn Ser Thr Leu Gly Ser Gly Phe Ile Leu Val Gly
  1              5              10              15

Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Tyr Ala Thr Phe Thr
      20              25              30

Ile Leu Tyr Met Leu Ala Leu Thr Ser Asn Gly Leu Leu Leu Leu Ala
      35              40              45

Ile Thr Ile Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
      50              55              60

Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
      65              70              75              80

Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
      85              90              95

Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Ser Ala Glu Asp
      100             105             110

Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115             120             125

Pro Leu Lys Tyr Met Thr Leu Met Ser Pro Arg Val Cys Trp Ile Met
      130             135             140

Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ile Ala Ile Gly His Thr
      145             150             155             160

Met Tyr Thr Met His Leu Pro Phe Cys Val Ser Trp Glu Ile Arg His
      165             170             175

Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
      180             185             190

Ser Arg Tyr Glu Leu Ile Ile Tyr Val Thr Gly Val Thr Phe Leu Leu
      195             200             205

Leu Pro Ile Ser Ala Ile Val Ala Ser Tyr Thr Leu Val Leu Phe Thr
      210             215             220

Val Leu Arg Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
      225             230             235             240

Cys Ser Ser His Leu Ile Val Val Gly Met Phe Tyr Gly Ala Ala Thr
      245             250             255

Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn
      260             265             270

Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu

```

275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
 290 295 300
 Leu Gly Lys Tyr Ile Leu Leu Ala His Ser Thr Leu
 305 310 315

 <210> 3
 <211> 316
 <212> PRT
 <213> human

 <400> 3
 Met Glu Leu Trp Asn Phe Thr Leu Gly Ser Gly Phe Ile Leu Val Gly
 1 5 10 15
 Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Ile Thr
 20 25 30
 Ile Leu Tyr Leu Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Ala
 35 40 45
 Ile Thr Met Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
 50 55 60
 Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
 65 70 75 80
 Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
 85 90 95
 Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Gly Ala Glu Asp
 100 105 110
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Thr Tyr Met Thr Leu Met Ser Ser Arg Ala Cys Trp Leu Met
 130 135 140
 Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Ile Tyr Thr
 145 150 155 160
 Val Tyr Thr Met His Tyr Pro Phe Cys Arg Ala Gln Glu Ile Arg His
 165 170 175
 Leu Leu Cys Glu Ile Pro His Leu Leu Lys Val Ala Cys Ala Asp Thr
 180 185 190
 Ser Arg Tyr Glu Leu Met Val Tyr Val Met Gly Val Thr Phe Leu Ile
 195 200 205
 Pro Ser Leu Ala Ala Ile Leu Ala Ser Tyr Thr Gln Ile Leu Leu Thr
 210 215 220

Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Ala Ala Thr
 245 250 255
 Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
 290 295 300
 Leu Gly Lys Tyr Met Leu Pro Ala His Ser Thr Leu
 305 310 315

<210> 4
 <211> 316
 <212> PRT
 <213> mouse

<400> 4
 Met Glu Leu Trp Asn Ser Thr Leu Glu Ser Gly Phe Ile Leu Val Gly
 1 5 10 15
 Ile Leu Asn Gly Ser Ser Ser Pro Glu Leu Leu Cys Ala Ile Val Thr
 20 25 30
 Ala Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Leu Val
 35 40 45
 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg
 50 55 60
 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
 65 70 75 80
 Ala Val Met Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Gly Gly
 85 90 95
 Cys Ala Leu Gln Met Ala Leu Ala Leu Met Leu Gly Ser Ala Glu Asp
 100 105 110
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Asn Tyr Met Val Phe Met Ser Pro Thr Val Cys Trp Leu Ile
 130 135 140
 Val Ser Thr Ser Trp Ile Leu Ala Ser Leu Thr Ala Val Gly His Thr
 145 150 155 160
 Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His
 165 170 175

Leu Leu Cys Glu Ile Leu Pro Leu Leu Lys Leu Ser Cys Val Asp Thr
 180 185 190
 Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Thr Phe Leu Leu
 195 200 205
 Leu Pro Leu Ser Ala Ile Val Thr Ser Tyr Thr Leu Ile Leu Ser Thr
 210 215 220
 Val Leu His Met Pro Ser Asn Glu Gly Lys Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Leu Ser His Leu Met Val Val Gly Met Phe Tyr Gly Ala Ala Thr
 245 250 255
 Phe Met Tyr Val Leu Pro Ser Ser Leu His Ser Ala Lys Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Leu Arg Arg Val
 290 295 300
 Leu Gly Arg Tyr Ile Leu Pro Ala His Leu Thr Leu
 305 310 315

<210> 5
 <211> 316
 <212> PRT
 <213> mouse

<400> 5
 Met Glu Pro Trp Asn Ser Thr Leu Glu Ser Gly Phe Ile Leu Val Gly
 1 5 10 15
 Ile Leu Asp Gly Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Val Thr
 20 25 30
 Thr Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Leu Val
 35 40 45
 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg
 50 55 60
 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Asn
 65 70 75 80
 Thr Val Val Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly
 85 90 95
 Cys Ala Leu Gln Leu Phe Ser Ala Met Thr Leu Gly Gly Ala Glu Asp
 100 105 110
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His

115		120		125
Pro Leu Asn Tyr Met Ile Phe Met Ser Pro Lys Ala Cys Arg Leu Met				
130		135		140
Val Ala Ile Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Gly His Thr				
145		150		155
Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His				
		165		170
Leu Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr				
		180		185
Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Ile Phe Leu Leu				
		195		200
Leu Pro Leu Ser Ala Ile Ile Thr Ser Tyr Ser Leu Ile Leu Phe Thr				
		210		215
Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr				
		225		230
Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Gly Ala Thr				
		245		250
Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn				
		260		265
Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu				
		275		280
Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Val Arg Arg Val				
		290		295
Leu Gly Arg His Ile Leu Pro Ala His Ala Thr Val				
		305		310

<210> 6
 <211> 316
 <212> PRT
 <213> mouse

<400> 6
Met Glu Pro Trp Asn Ser Thr Leu Glu Ser Gly Phe Ile Leu Val Gly
1 5 10 15
Ile Leu Asp Gly Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Val Thr
20 25 30
Thr Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Val
35 40 45
Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg
50 55 60

Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Asn
 65 70 75 80
 Thr Val Val Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly
 85 90 95
 Cys Ala Leu Gln Leu Phe Ser Ala Met Thr Leu Gly Gly Ala Glu Glu
 100 105 110
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Asn Tyr Met Ile Phe Met Ser Pro Lys Ala Cys Arg Leu Met
 130 135 140
 Val Ala Ile Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Gly His Thr
 145 150 155 160
 Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His
 165 170 175
 Leu Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
 180 185 190
 Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Ile Phe Leu Leu
 195 200 205
 Leu Pro Leu Ser Ala Ile Ile Thr Ser Tyr Ser Leu Ile Leu Phe Thr
 210 215 220
 Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Gly Ala Thr
 245 250 255
 Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Val Arg Arg Val
 290 295 300
 Leu Gly Arg His Ile Leu Pro Ala His Ala Thr Val
 305 310 315

<210> 7
 <211> 316
 <212> PRT
 <213> mouse

<400> 7
 Met Glu Pro Trp Asn Ser Thr Leu Gly Thr Asp Phe Asn Leu Val Gly
 1 5 10 15

Ile Leu Asp Asp Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Phe Thr
 20 25 30
 Ala Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Ile Leu Val
 35 40 45
 Ile Thr Met Asp Ala Arg Leu His Val Pro Met Tyr Phe Leu Leu Gly
 50 55 60
 Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
 65 70 75 80
 Ala Val Ile Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly
 85 90 95
 Cys Ser Leu Gln Met Phe Leu Ala Leu Thr Leu Gly Gly Ala Glu Asp
 100 105 110
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Asn Tyr Met Ile Phe Met Arg Pro Ser Ile Cys Trp Leu Met
 130 135 140
 Val Ala Thr Ser Trp Val Leu Ala Ser Leu Met Ala Leu Gly Tyr Thr
 145 150 155 160
 Thr Tyr Thr Met Gln Tyr Ser Tyr Cys Lys Ser Arg Lys Ile Arg His
 165 170 175
 Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
 180 185 190
 Ser Lys Tyr Glu Leu Met Val Tyr Val Met Gly Val Thr Phe Leu Ile
 195 200 205
 Pro Pro Leu Ala Ala Ile Leu Ala Ser Tyr Ser Leu Ile Leu Phe Thr
 210 215 220
 Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Ala Ala Thr
 245 250 255
 Phe Met Tyr Val Leu Pro Asn Ser Phe His Ser Pro Arg Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Leu Ile Arg Val
 290 295 300
 Leu Gly Arg Tyr Ile Val Pro Ala His Pro Thr Leu
 305 310 315

<210> 8
 <211> 17
 <212> PRT
 <213> Unknown Organism

 <220>
 <223> Description of Unknown Organism: Protein motif

 <220>
 <221> MISC_FEATURE
 <222> (1)
 <223> X1 wherein Xaa is Gly, or Ser, or Thr, or Ala, or Leu, or
 Ile, or Val, or Met, or Phe, or Tyr, or Trp, or Cys

 <220>
 <221> MISC_FEATURE
 <222> (2)
 <223> X2 wherein Xaa is Gly, or Ser, or Thr, or Ala, or Asn, or
 Cys, or Pro, or Asp, or Glu

 <220>
 <221> MISC_FEATURE
 <222> (3)
 <223> X3 wherein Xaa is Glu, or Asp, or Pro, or Lys, or Arg, or His

 <220>
 <221> MISC_FEATURE
 <222> (4)
 <223> X4 wherein Xaa is any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (5)
 <223> X5 wherein Xaa is any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (6)
 <223> X6 wherein Xaa is Leu, or Ile, or Val, or Met, or Asn, or
 Gln, or Gly, or Ala

 <220>
 <221> MISC_FEATURE
 <222> (7)
 <223> X7 wherein Xaa is any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (8)
 <223> X8 wherein Xaa is any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (9)
 <223> X9 wherein Xaa is Leu, or Ile, or Val, or Met, or Phe, or Thr

<220>
 <221> MISC_FEATURE
 <222> (10)
 <223> X10 wherein Xaa is Gly, or Ser, or Thr, or Ala, or Asn, or Cys

<220>
 <221> MISC_FEATURE
 <222> (11)
 <223> X11 wherein Xaa is Leu, or Ile, or Val, or Met, or Phe, or Tyr, or Trp, or Ser, or Thr, or Ala, or Cys

<220>
 <221> MISC_FEATURE
 <222> (12)
 <223> X12 wherein Xaa is Asp, or Glu, or Asn, or His

<220>
 <221> MISC_FEATURE
 <222> (14)
 <223> X13 wherein Xaa is Phe, or Tyr, or Trp, or Cys, or Ser, or His

<220>
 <221> MISC_FEATURE
 <222> (15)
 <223> X14 wherein Xaa is any amino acid

<220>
 <221> MISC_FEATURE
 <222> (16)
 <223> X15 wherein Xaa is any amino acid

<220>
 <221> MISC_FEATURE
 <222> (17)
 <223> X16 wherein Xaa is Leu, or Ile or Val, or Met

<400> 8
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa
 1 5 10 15

Xaa

<210> 9
 <211> 254
 <212> PRT
 <213> Unknown Organism

<220>
 <221> DOMAIN
 <222> (1)..(254)
 <223> 7tm_1,7 transmembrane receptor domain

<400> 9

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg
 1 5 10 15
 Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu
 20 25 30
 Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
 35 40 45
 Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe
 50 55 60
 Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile
 65 70 75 80
 Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg
 85 90 95
 Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala
 100 105 110
 Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val
 115 120 125
 Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser
 130 135 140
 Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Val Leu
 145 150 155 160
 Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu
 165 170 175
 Arg Lys Arg Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser
 180 185 190
 Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Val Phe Val
 195 200 205
 Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys
 210 215 220
 Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu
 225 230 235 240
 Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr
 245 250

<210> 10

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> .10
tgccacattc atgtatgtct tg. 22

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 11
cacagcccca aacaagacaa catcat 26

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 12
ggctggagtg acaattgtgt ag 22